

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/563,074
Source: ITWIP
Date Processed by STIC: 1-13-06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/13/2006

PATENT APPLICATION: US/10/563,074

TIME: 10:26:00

Input Set : A:\Sequence Listing 3190-087.txt

Output Set: N:\CRF4\01132006\J563074.raw

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3 <110> APPLICANT: WADA,Naoya
4      OKAMOTO, Takashi
5      TANIGAKI, Keiji
6      DOI, Hirofumi
7      KIKUCHI, Yasuhiro
8      IMAI, Kensaku
10 <120> TITLE OF INVENTION: Method for Inhibiting Telomerase Activity and Inhibitor
Thereof
12 <130> FILE REFERENCE: 3190-087
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/563,074
15 <141> CURRENT FILING DATE: 2005-12-29
17 <150> PRIOR APPLICATION NUMBER: JP P2004-143902
18 <151> PRIOR FILING DATE: 2004-05-13
20 <150> PRIOR APPLICATION NUMBER: PCT/JP2005/008239
21 <151> PRIOR FILING DATE: 2005-04-28
23 <160> NUMBER OF SEQ ID NOS: 13
25 <170> SOFTWARE: PatentIn version 3.1
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1149
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1149)
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <223> OTHER INFORMATION: A polynucleotide encoding MAPKAPK3 (SEQ ID NO:2)
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44 Met Asp Gly Glu Thr Ala Glu Glu Gln Gly Gly Pro Val Pro Pro Pro
45 1          5          10          15
47 gtt gca ccc ggc gga ccc ggc ttg ggc ggt gct ccg ggg ggg cgg cgg      96
48 Val Ala Pro Gly Gly Pro Gly Leu Gly Gly Ala Pro Gly Gly Arg Arg
49          20          25          30
51 gag ccc aag aag tac gca gtg acc gac gac tac cag ttg tcc aag cag      144
52 Glu Pro Lys Lys Tyr Ala Val Thr Asp Asp Tyr Gln Leu Ser Lys Gln
53          35          40          45
55 gtg ctg ggc ctg ggt gtg aac ggc aaa gtg ctg gag tgc ttc cat cgg      192
56 Val Leu Gly Leu Gly Val Asn Gly Lys Val Leu Glu Cys Phe His Arg
57          50          55          60
59 cgc act gga cag aag tgt gcc ctg aag ctc ctg tat gac agc ccc aag      240
60 Arg Thr Gly Gln Lys Cys Ala Leu Lys Leu Leu Tyr Asp Ser Pro Lys
61 65          70          75          80
63 gcc cgg cag gag gta gac cat cac tgg cag gct tct ggc ggc ccc cat      288

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64 Ala Arg Gln Glu Val Asp His His Trp Gln Ala Ser Gly Gly Pro His
65                               85                               90                               95
67 att gtc tgc atc ctg gat gtg tat gag aac atg cac cat ggc aag cgc      336
68 Ile Val Cys Ile Leu Asp Val Tyr Glu Asn Met His His Gly Lys Arg
69                               100                               105                               110
71 tgt ctc ctc atc atc atg gaa tgc atg gaa ggt ggt gag ttg ttc agc      384
72 Cys Leu Leu Ile Ile Met Glu Cys Met Glu Gly Gly Glu Leu Phe Ser
73                               115                               120                               125
75 agg att cag gag cgt ggc gac cag gct ttc act gag aga gaa gct gca      432
76 Arg Ile Gln Glu Arg Gly Asp Gln Ala Phe Thr Glu Arg Glu Ala Ala
77                               130                               135                               140
79 gag ata atg cgg gat att ggc act gcc atc cag ttt ctg cac agc cat      480
80 Glu Ile Met Arg Asp Ile Gly Thr Ala Ile Gln Phe Leu His Ser His
81 145                               150                               155                               160
83 aac att gcc cac cga gat gtc aag cct gaa aac cta ctc tac aca tct      528
84 Asn Ile Ala His Arg Asp Val Lys Pro Glu Asn Leu Leu Tyr Thr Ser
85                               165                               170                               175
87 aag gag aaa gac gca gtg ctt aag ctc acc gat ttt ggc ttt gct aag      576
88 Lys Glu Lys Asp Ala Val Leu Lys Leu Thr Asp Phe Gly Phe Ala Lys
89                               180                               185                               190
91 gag acc acc caa aat gcc ctg cag aca ccc tgc tat act ccc tat tat      624
92 Glu Thr Thr Gln Asn Ala Leu Gln Thr Pro Cys Tyr Thr Pro Tyr Tyr
93                               195                               200                               205
95 gtg gcc cct gag gtc ctg ggt cca gag aag tat gac aag tca tgt gac      672
96 Val Ala Pro Glu Val Leu Gly Pro Glu Lys Tyr Asp Lys Ser Cys Asp
97                               210                               215                               220
99 atg tgg tcc ctg ggt gtc atc atg tac atc ctc ctt tgt ggc ttc cca      720
100 Met Trp Ser Leu Gly Val Ile Met Tyr Ile Leu Leu Cys Gly Phe Pro
101 225                               230                               235                               240
103 ccc ttc tac tcc aac acg ggc cag gcc atc tcc ccg ggg atg aag agg      768
104 Pro Phe Tyr Ser Asn Thr Gly Gln Ala Ile Ser Pro Gly Met Lys Arg
105                               245                               250                               255
107 agg att cgc ctg ggc cag tac ggc ttc ccc aat cct gag tgg tca gaa      816
108 Arg Ile Arg Leu Gly Gln Tyr Gly Phe Pro Asn Pro Glu Trp Ser Glu
109                               260                               265                               270
111 gtc tct gag gat gcc aag cag ctg atc cgc ctc ctg ttg aag aca gac      864
112 Val Ser Glu Asp Ala Lys Gln Leu Ile Arg Leu Leu Leu Lys Thr Asp
113                               275                               280                               285
115 ccc aca gag agg ctg acc atc act cag ttc atg aac cac ccc tgg atc      912
116 Pro Thr Glu Arg Leu Thr Ile Thr Gln Phe Met Asn His Pro Trp Ile
117                               290                               295                               300
119 aac caa tcg atg gta gtg cca cag acc cca ctc cac acg gcc cga gtg      960
120 Asn Gln Ser Met Val Val Pro Gln Thr Pro Leu His Thr Ala Arg Val
121 305                               310                               315                               320
123 ctg cag gag gac aaa gac cac tgg gac gaa gtc aag gag gag atg acc      1008
124 Leu Gln Glu Asp Lys Asp His Trp Asp Glu Val Lys Glu Glu Met Thr
125                               325                               330                               335
127 agt gcc ttg gcc act atg cgg gta gac tac gac cag gtg aag atc aag      1056
128 Ser Ala Leu Ala Thr Met Arg Val Asp Tyr Asp Gln Val Lys Ile Lys

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129          340          345          350
131 gac ctg aag acc tct aac aac cgg ctc ctc aac aag agg aga aaa aag      1104
132 Asp Leu Lys Thr Ser Asn Asn Arg Leu Leu Asn Lys Arg Arg Lys Lys
133          355          360          365
135 cag gca ggc agc tcc tct gcc tca cag ggc tgc aac aac cag tag      1149
136 Gln Ala Gly Ser Ser Ser Ala Ser Gln Gly Cys Asn Asn Gln
137          370          375          380
140 <210> SEQ ID NO: 2
141 <211> LENGTH: 382
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
145 <400> SEQUENCE: 2
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148 1          5          10          15
151 Val Ala Pro Gly Gly Pro Gly Leu Gly Gly Ala Pro Gly Gly Arg Arg
152          20          25          30
155 Glu Pro Lys Lys Tyr Ala Val Thr Asp Asp Tyr Gln Leu Ser Lys Gln
156          35          40          45
159 Val Leu Gly Leu Gly Val Asn Gly Lys Val Leu Glu Cys Phe His Arg
160          50          55          60
163 Arg Thr Gly Gln Lys Cys Ala Leu Lys Leu Leu Tyr Asp Ser Pro Lys
164 65          70          75          80
167 Ala Arg Gln Glu Val Asp His His Trp Gln Ala Ser Gly Gly Pro His
168          85          90          95
171 Ile Val Cys Ile Leu Asp Val Tyr Glu Asn Met His His Gly Lys Arg
172          100          105          110
175 Cys Leu Leu Ile Ile Met Glu Cys Met Glu Gly Gly Glu Leu Phe Ser
176          115          120          125
179 Arg Ile Gln Glu Arg Gly Asp Gln Ala Phe Thr Glu Arg Glu Ala Ala
180          130          135          140
183 Glu Ile Met Arg Asp Ile Gly Thr Ala Ile Gln Phe Leu His Ser His
184 145          150          155          160
187 Asn Ile Ala His Arg Asp Val Lys Pro Glu Asn Leu Leu Tyr Thr Ser
188          165          170          175
191 Lys Glu Lys Asp Ala Val Leu Lys Leu Thr Asp Phe Gly Phe Ala Lys
192          180          185          190
195 Glu Thr Thr Gln Asn Ala Leu Gln Thr Pro Cys Tyr Thr Pro Tyr Tyr
196          195          200          205
199 Val Ala Pro Glu Val Leu Gly Pro Glu Lys Tyr Asp Lys Ser Cys Asp
200          210          215          220
203 Met Trp Ser Leu Gly Val Ile Met Tyr Ile Leu Leu Cys Gly Phe Pro
204 225          230          235          240
207 Pro Phe Tyr Ser Asn Thr Gly Gln Ala Ile Ser Pro Gly Met Lys Arg
208          245          250          255
211 Arg Ile Arg Leu Gly Gln Tyr Gly Phe Pro Asn Pro Glu Trp Ser Glu
212          260          265          270
215 Val Ser Glu Asp Ala Lys Gln Leu Ile Arg Leu Leu Leu Lys Thr Asp
216          275          280          285
219 Pro Thr Glu Arg Leu Thr Ile Thr Gln Phe Met Asn His Pro Trp Ile

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220      290      295      300
223 Asn Gln Ser Met Val Val Pro Gln Thr Pro Leu His Thr Ala Arg Val
224 305      310      315      320
227 Leu Gln Glu Asp Lys Asp His Trp Asp Glu Val Lys Glu Glu Met Thr
228      325      330      335
231 Ser Ala Leu Ala Thr Met Arg Val Asp Tyr Asp Gln Val Lys Ile Lys
232      340      345      350
235 Asp Leu Lys Thr Ser Asn Asn Arg Leu Leu Asn Lys Arg Arg Lys Lys
236      355      360      365
239 Gln Ala Gly Ser Ser Ser Ala Ser Gln Gly Cys Asn Asn Gln
240      370      375      380
243 <210> SEQ ID NO: 3
244 <211> LENGTH: 3399
245 <212> TYPE: DNA
246 <213> ORGANISM: Homo sapiens
248 <220> FEATURE:
249 <221> NAME/KEY: CDS
250 <222> LOCATION: (1)..(3399)
253 <220> FEATURE:
254 <221> NAME/KEY: misc_feature
255 <223> OTHER INFORMATION: A polynucleotide encoding TERT (SEQ ID NO:4)
258 <400> SEQUENCE: 3
259 atg ccg cgc gct ccc cgc tgc cga gcc gtg cgc tcc ctg ctg cgc agc      48
260 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
261 1      5      10      15
263 cac tac cgc gag gtg ctg ccg ctg gcc acg ttc gtg cgg cgc ctg ggg      96
264 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
265      20      25      30
267 ccc cag ggc tgg cgg ctg gtg cag cgc ggg gac ccg gcg gct ttc cgc      144
268 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
269      35      40      45
271 gcg ctg gtg gcc cag tgc ctg gtg tgc gtg ccc tgg gac gca cgg ccg      192
272 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
273      50      55      60
275 ccc ccc gcc gcc ccc tcc ttc cgc cag gtg tcc tgc ctg aag gag ctg      240
276 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
277 65      70      75      80
279 gtg gcc cga gtg ctg cag agg ctg tgc gag cgc ggc gcg aag aac gtg      288
280 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
281      85      90      95
283 ctg gcc ttc ggc ttc gcg ctg ctg gac ggg gcc cgc ggg ggc ccc ccc      336
284 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
285      100      105      110
287 gag gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc      384
288 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
289      115      120      125
291 gac gca ctg cgg ggg agc ggg gcg tgg ggg ctg ctg ctg cgc cgc gtg      432
292 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
293      130      135      140

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295	ggc	gac	gac	gtg	ctg	gtt	cac	ctg	ctg	gca	cgc	tgc	gcg	ctc	ttt	gtg	480
296	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	
297	145					150					155					160	
299	ctg	gtg	gct	ccc	agc	tgc	gcc	tac	cag	gtg	tgc	ggg	ccg	ccg	ctg	tac	528
300	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	
301					165					170						175	
303	cag	ctc	ggc	gct	gcc	act	cag	gcc	cgg	ccc	ccg	cca	cac	gct	agt	gga	576
304	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	
305				180					185					190			
307	ccc	cga	agg	cgt	ctg	gga	tgc	gaa	cgg	gcc	tgg	aac	cat	agc	gtc	agg	624
308	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	
309			195					200				205					
311	gag	gcc	ggg	gtc	ccc	ctg	ggc	ctg	cca	gcc	ccg	ggt	gcg	agg	agg	cgc	672
312	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	
313		210					215					220					
315	ggg	ggc	agt	gcc	agc	cga	agt	ctg	ccg	ttg	ccc	aag	agg	ccc	agg	cgt	720
316	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	
317	225					230				235						240	
319	ggc	gct	gcc	cct	gag	ccg	gag	cgg	acg	ccc	gtt	ggg	cag	ggg	tcc	tgg	768
320	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	
321					245					250						255	
323	gcc	cac	ccg	ggc	agg	acg	cgt	gga	ccg	agt	gac	cgt	ggt	ttc	tgt	gtg	816
324	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	
325				260					265					270			
327	gtg	tca	cct	gcc	aga	ccc	gcc	gaa	gaa	gcc	acc	tct	ttg	gag	ggt	gcg	864
328	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	
329			275					280					285				
331	ctc	tct	ggc	acg	cgc	cac	tcc	cac	cca	tcc	gtg	ggc	cgc	cag	cac	cac	912
332	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	
333		290					295					300					
335	gcg	ggc	ccc	cca	tcc	aca	tcg	cgg	cca	cca	cgt	ccc	tgg	gac	acg	cct	960
336	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	
337	305					310					315					320	
339	tgt	ccc	ccg	gtg	tac	gcc	gag	acc	aag	cac	ttc	ctc	tac	tcc	tca	ggc	1008
340	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	
341					325					330						335	
343	gac	aag	gag	cag	ctg	cgg	ccc	tcc	ttc	cta	ctc	agc	tct	ctg	agg	ccc	1056
344	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	
345				340					345					350			
347	agc	ctg	act	ggc	gct	cgg	agg	ctc	gtg	gag	acc	atc	ttt	ctg	ggt	tcc	1104
348	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	
349			355					360					365				
351	agg	ccc	tgg	atg	cca	ggg	act	ccc	cgc	agg	ttg	ccc	cgc	ctg	ccc	cag	1152
352	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	
353		370					375					380					
355	cgc	tac	tgg	caa	atg	cgg	ccc	ctg	ttt	ctg	gag	ctg	ctt	ggg	aac	cac	1200
356	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	
357	385					390					395					400	
359	gcg	cag	tgc	ccc	tac	ggg	gtg	ctc	ctc	aag	acg	cac	tgc	ccg	ctg	cga	1248

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/13/2006
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number